Listing of the Claims

1. (currently amended) A method ~~and system~~ for simultaneous analysis of <u>biological</u> samples, comprising:

    obtaining a number of <u>biological</u> samples to be analyzed;

    extracting RNA from each said sample to be analyzed;

    isolating mRNA from said RNA to use as a template for synthesizing DNA;

    synthesizing cDNA from each said mRNA of each said sample;

    labeling each said cDNA with a label;

    depositing an array of known reagents into as many wells of a <u>glass bottom</u> multi-well microtiter plate platform as desired for a particular assay and immobilizing each said array <u>to said glass bottom thereof</u> ~~thereon~~;

    depositing at least one of said labeled cDNA into at least one well of said multi-well microtiter plate platform;

    depositing at least one said labeled cDNA into as many said wells having a said array therein as desired for a particular assay;

    allowing said each said labeled cDNA to hybridize to said array of known reagents in each said well;

    reading said microtiter plate platform after hybridization is completed; and

    using software, processing signals generated and read from said at least one label into a format useful for analysis.

2. (currently amended) The method according to claim 1 wherein said number of <u>biological</u> samples to be assayed simultaneously is at least about 6.

3. (currently amended) The method according to claim 1 wherein said <u>biological</u> samples are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

4. (original) The method according to claim 1 wherein said label is chosen from the group consisting of: a fluorescent label, a radio label, a colorimetric label, or a reflective label.

5. (original) The method according to claim 4 wherein said reading is performed on a device capable of reading a signal chosen from the group consisting of: fluorescence, radioactivity, color intensity, and reflection changes.

6. (currently amended) The method of claim 1 wherein two biological samples are deposited in each well of said microtiter plate platform.

7. (currently amended) The method of claim 6 wherein each of said two biological samples is labeled with a different label of the same type.

8. (original) The method of claim 7 wherein said reading is performed using a device capable of simultaneously reading two of the same type of signals.

9. (currently amended) A method and system of parallel analysis of biological samples simultaneously, comprising:

obtaining a number of biological samples to be analyzed;

extracting RNA from each said sample to be analyzed;

isolating mRNA from said RNA to use as a template for synthesizing DNA;

synthesizing cDNA from each said mRNA of each said sample;

labeling each said cDNA with a label;

depositing an array of known reagents into as many wells of a glass bottom multi-well microtiter plate platform as desired for a particular assay and immobilizing each said array to said glass bottom thereof thereon;

depositing one of said labeled cDNA into a well of said multi-well microtiter plate platform;

depositing one said labeled cDNA into as many said wells having a said array therein as desired for a particular assay;

allowing said each said labeled cDNA to hybridize to said array of known reagents;

reading said microtiter plate platform after hybridization is completed; and

using software, processing signals generated and read from said label into a format useful for analysis.

10. (currently amended) The method according to claim 9 wherein said number of biological samples to be assayed simultaneously is at least about 6.

11. (currently amended) The method according to claim 9 wherein said <u>biological</u> samples are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

12. (original) The method according to claim 9 wherein said label is chosen from the group consisting of: a fluorescent label, a radio label, a colorimetric label, and a reflective label.

13. (original) The method according to claim 12 wherein said reading is performed on a device capable of reading a signal chosen from the group consisting of: fluorescence, radioactivity, color intensity and reflection changes.

14. (currently amended) The method according to claim 9 wherein each said <u>cDNA from each said biological</u> sample is labeled with the same said label.

15. (currently amended) A method for multiple parallel analysis of <u>biological</u> samples simultaneously, comprising:

obtaining a number of <u>biological</u> samples to be analyzed;

extracting RNA from each said sample to be analyzed;

isolating mRNA from said RNA to use as a template for synthesizing DNA;

synthesizing cDNA from each said mRNA of each said sample;

labeling each said cDNA with one of either a first or a second label<u>, said first and said second labels being of the same type of label</u>;

depositing an array of known reagents into as many wells of a multi-well microtiter plate platform as desired for a particular assay and immobilizing each said array <u>to said glass bottom thereof</u> <s>thereon</s>;

depositing one said cDNA labeled with said first label, and one said cDNA labeled with said second label into the same well of said multi-well microtiter plate platform;

depositing both a said cDNA labeled with said first label and a said cDNA labeled with said second label in as many wells having a said array therein as desired for a particular assay;

allowing said both said labeled cDNAs to hybridize to said array of known reagents in each said well;

reading said microtiter plate platform after hybridization is completed; and

using software, processing signals generated and read from said first and said second labels into a format useful for analysis.

16. (currently amended) The method according to claim 15 wherein said number of <u>biological</u> samples to be assayed simultaneously is at least about 6.

17. (currently amended) The method according to claim 15 wherein said <u>biological</u> samples are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

18. (original) The method according to claim 15 wherein said first and said second labels are chosen from the group consisting of: a fluorescent label, a radio label, a colorimetric label, and a reflective label.

19. (original) The method according to claim 15 wherein said reading is performed on a device capable of reading simultaneously two of the same type of signals chosen from the group consisting of: fluorescence, radioactivity, color intensity, and reflection changes.

20. (currently amended) The method according to claim 1 wherein a universal or other control sample<u>, having the same label as said labeled cDNA,</u> is deposited in at least one well of said microtiter plate platform, <s>for use</s> as an intra-well and inter-well normalization tool, to define background and align image for reading said microtiter plate platform.

21. (currently amended) The method according to claim 9 wherein a universal or other control sample<u>, having the same label as said labeled cDNA,</u> is deposited in at least one well of said microtiter plate platform, <s>for use</s> as an intra-well and inter-well normalization tool, and to define background and align image for reading said microtiter plate platform.

22. (currently amended) The method according to claim 15 wherein a universal or other control sample<u>, having said first label,</u> is deposited in at least one well of said microtiter plate platform, <s>for use</s> as an intra-well and inter-well normalization tool and to define background and align image for reading said microtiter plate platform<u>, and a universal or other control sample, having said second label, is deposited in at least one well of said microtiter plate platform as an intra-well and inter-well normalization tool and to define background and align image for reading said microtiter plate platform.</u>

23. (original) The method of claim 1 wherein said array of known reagents is deposited on the inner bottom surface of said well on an area in the maximum range of about 2.25mm x 2.25mm to about 36.0mm x 36.0mm, said area being dependent upon the number and size of wells formed in said microtiter plate platform and the density of the array deposited therein.

24. (original) The method of claim 9 wherein said array of known reagents is deposited on the inner bottom surface of said well on an area in the maximum range of about 2.25mm x 2.25mm to about 36.0mm x 36.0mm, said area being dependent upon the number and size of wells formed in said microtiter plate platform and the density of the array deposited therein.

25. (original) The method of claim 15 wherein said array of known reagents is deposited on the inner bottom surface of said well on an area in the maximum range of about 2.25mm x 2.25mm to about 36.0mm x 36.0mm, said area being dependent upon the number and size of wells formed in said microtiter plate platform and the density of the array deposited therein.

26. (original) The method of claim 23 wherein said inner bottom surface of each said well is glass.

27. (original) The method of claim 24 wherein said inner bottom surface of each said well is glass.

28. (original) The method of claim 25 wherein said inner bottom surface of each said well is glass.

29. (currently amended) A method ~~and system~~ for multiple parallel analysis of <u>biological</u> samples simultaneously, comprising:

depositing an array of known reagents into as many wells of a <u>glass bottom</u> multi-well microtiter plate platform as desired for a particular assay and immobilizing each said array <u>to said glass bottom thereof</u> ~~thereon~~;

depositing at least one labeled cDNA <u>sample</u> into at least one well of said multi-well microtiter plate platform;

depositing at least one said labeled cDNA <u>sample</u> into as many wells having a said array therein as desired for a particular assay;

allowing said each said labeled cDNA <u>sample</u> to hybridize to said array of known reagents in each said well;

reading said microtiter plate platform after hybridization is completed; and

using software, processing signals generated and read from said at least one label into a format useful for analysis.

30. (new) The method according to claim 1 wherein said known reagents are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

31. (new) The method according to claim 9 wherein said known reagents are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

32. (new) The method according to claim 15 wherein said known reagents are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

33. (new) A system for simultaneous analysis of biological samples comprising:

a glass bottom multi-well microtiter plate platform;

a fluid-handling device to deposit an array of known reagents in at least one well of said glass bottom multi-well microtiter plate platform, wherein said array is immobilized on said glass bottom of said multi-well microtiter plate platform;

a fluid-handling device to deposit at least one labeled biological sample into at least one well of said glass bottom multi-well microtiter plate platform for reaction with said array; and a microtiter plate reader to detect said label and thus any reaction between said known reagents of said array and said at least one labeled biological sample to yield assay results.

34. (new) The system according to claim 33 comprising a computer with software to process signals generated from said label into a format useful for analysis.

35. (new) The system according to claim 33 wherein said biological samples are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.

36. (new) The system according to claim 33 wherein said known reagents are chosen from the group consisting of: DNA, RNA, PNA, genes, portions of genes, polynucleotides, polypeptide biopolymers, fragments of DNA, fragments of RNA, short oligonucleotides, proteins and polypeptides.